

(2)

OIKE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/900,766

DATE: 07/24/2001.  
 TIME: 10:47:32

Input Set : A:\Seq.txt  
 Output Set: N:\CRF3\07242001\I900766.raw

ENTERED

3 <110> APPLICANT: FORSBERG, GORAN  
 4 ERLANDSSON, EVA  
 5 ANTONSSON, PER  
 6 WALSE, BJORN  
 8 <120> TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY  
 10 <130> FILE REFERENCE: P02188US0;10104199  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/900,766  
 C--> 13 <141> CURRENT FILING DATE: 2001-07-06  
 15 <160> NUMBER OF SEQ ID NOS: 7  
 17 <170> SOFTWARE: PatentIn version 3.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 672  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: PEPTIDE  
 26 <222> LOCATION: (1)..(672)  
 27 <223> OTHER INFORMATION: Conjugate protein  
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 32 Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala  
 33 1 5 10 15  
 35 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr  
 36 20 25 30  
 38 Tyr Met His Trp Val Lys Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile  
 39 35 40 45  
 41 Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe  
 42 50 55 60  
 44 Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr  
 45 65 70 75 80  
 47 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
 48 85 90 95  
 50 Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln  
 51 100 105 110  
 53 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val  
 54 115 120 125  
 56 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr  
 57 130 135 140  
 59 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr  
 60 145 150 155 160  
 62 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val  
 63 165 170 175  
 65 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser  
 66 180 185 190  
 68 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala  
 69 195 200 205  
 71 Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Ser Gly Gly  
 72 210 215 220

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74 Pro Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys
75 225                230                235                240
77 Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr
78                245                250                255
80 Tyr Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe
81                260                265                270
83 Leu Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp
84                275                280                285
86 Tyr Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu
87                290                295                300
89 Tyr Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln
90 305                310                315                320
92 Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val
93                325                330                335
95 Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile
96                340                345                350
98 Asn Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val
99                355                360                365
101 Lys Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala
102                370                375                380
104 Arg His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe
105 385                390                395                400
107 Gly Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly
108                405                410                415
110 Ser Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp
111                420                425                430
113 Thr Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser
114                435                440                445
116 Leu Ser Ile Ser Leu Tyr Leu Tyr Thr Thr Ser Ile Val Met Thr Gln
117                450                455                460
119 Thr Pro Thr Ser Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr
120 465                470                475                480
122 Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln
123                485                490                495
125 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Thr Ser Ser Arg
126                500                505                510
128 Tyr Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp
129                515                520                525
131 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Val Tyr
132                530                535                540
134 Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr
135 545                550                555                560
137 Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe
138                565                570                575
140 Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
141                580                585                590
143 Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
144                595                600                605
146 Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln

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147      610      615      620
149 Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
150 625      630      635      640
152 Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
153      645      650      655
155 Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Ser
156      660      665      670
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 233
160 <212> TYPE: PRT
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <221> NAME/KEY: Peptide
165 <222> LOCATION: (1)..(233)
166 <223> OTHER INFORMATION: Chimeric Protein
169 <400> SEQUENCE: 2
171 Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
172 1      5      10      15
174 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
175      20      25      30
177 Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe Leu
178      35      40      45
180 Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
181      50      55      60
183 Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu Tyr
184 65      70      75      80
186 Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
187      85      90      95
189 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
190      100      105      110
192 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
193      115      120      125
195 Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
196      130      135      140
198 Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
199 145      150      155      160
201 His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
202      165      170      175
204 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
205      180      185      190
207 Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
208      195      200      205
210 Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser Leu
211      210      215      220
213 Ser Ile Ser Leu Tyr Leu Tyr Thr Thr
214 225      230
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 233
218 <212> TYPE: PRT

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219 &lt;213&gt; ORGANISM: Artificial Sequence

221 &lt;220&gt; FEATURE:

222 &lt;221&gt; NAME/KEY: peptide

223 &lt;222&gt; LOCATION: (1)..(233)

224 &lt;223&gt; OTHER INFORMATION: Chimeric Protein

227 &lt;400&gt; SEQUENCE: 3

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229 Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
230 1          5          10          15
232 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
233          20          25          30
235 Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
236          35          40          45
238 Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
239          50          55          60
241 Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
242 65          70          75          80
244 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
245          85          90          95
247 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
248          100         105         110
250 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
251          115         120         125
253 Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
254          130         135         140
256 Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
257 145          150         155         160
259 His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
260          165         170         175
262 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
263          180         185         190
265 Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
266          195         200         205
268 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu
269          210         215         220
271 His Ile Ala Leu Tyr Leu Tyr Thr Thr
272 225          230

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274 &lt;210&gt; SEQ ID NO: 4

275 &lt;211&gt; LENGTH: 233

276 &lt;212&gt; TYPE: PRT

277 &lt;213&gt; ORGANISM: Staphylococcus sp.

279 &lt;400&gt; SEQUENCE: 4

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281 Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
282 1          5          10          15
284 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
285          20          25          30
287 Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu
288          35          40          45
290 Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp His Ser Trp Tyr
291          50          55          60

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```

293 Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr
294 65              70              75              80
296 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
297              85              90              95
299 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
300              100             105             110
302 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
303              115             120             125
305 Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys
306              130             135             140
308 Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
309 145              150             155             160
311 Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
312              165             170             175
314 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro
315              180             185             190
317 Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser Asn Thr
318              195             200             205
320 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met
321              210             215             220
323 His Ile Asp Ile Tyr Leu Tyr Thr Ser
324 225              230
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 203
328 <212> TYPE: PRT
329 <213> ORGANISM: Staphylococcus sp.
331 <400> SEQUENCE: 5
333 Ala Leu His Lys Lys Ser Glu Leu Ser Ser Thr Ala Leu Asn Asn Met
334 1              5              10              15
336 Lys His Ser Tyr Ala Asp Ala Asn Pro Ile Ile Gly Ala Asn Lys Ser
337              20              25              30
339 Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu Leu Tyr Lys Ala Phe Phe
340              35              40              45
342 Leu Leu Ile Asn Phe Asn Ser Ala Glu Met Ala Gln His Phe Lys Ser
343              50              55              60
345 Lys Asn Val Asp Val Tyr Ala Ile Arg Tyr Ala Ala Ala Cys Arg Thr
346 65              70              75              80
348 Ala Cys Thr Tyr Gly Gly Val Thr Pro His Ala Gly Asn Ala Leu Lys
349              85              90              95
351 Ala Arg Lys Lys Ile Pro Ile Asn Leu Trp Ile Ile Gly Val Gln Lys
352              100             105             110
354 Glu Val Ser Leu Asp Lys Val Gln Thr Asp Lys Lys Asn Val Thr Val
355              115             120             125
357 Gln Glu Leu Asp Ala Gln Ala Arg Arg Tyr Leu Gln Lys Asp Leu Lys
358              130             135             140
360 Leu Tyr Asn Ala Ile Gln Arg Gly Lys Leu Glu Phe Asp Ser Ala Ala
361 145              150             155             160
363 Ala Ser Lys Val Ser Tyr Asp Leu Phe Asp Val Ala Gly Asp Phe Pro
364              165             170             175

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,766

DATE: 07/24/2001

TIME: 10:47:33

Input Set : A:\Seq.txt

Output Set: N:\CRF3\07242001\I900766.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date